

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2002, 07:57:59 ; Search time 33.64 seconds
(without alignments)
1397,311 Million cell updates/sec

Title: US-09-783-320-4

Perfect score: 6243
Sequence: 1 NERKVRKRGKSGSFGKAIL.....YAKIHLVMDAGVQNDND 1214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105324 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105324

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3385	54.2	774	1	NERK1_MOUSE
2	847.5	13.6	841	1	STRK2_HUMAN
3	833	13.3	511	1	NERK3_MOUSE
4	790.5	12.7	439	1	NERK3_HUMAN
5	563.5	9.1	431	1	NERK4_HUMAN
6	543.5	8.9	443	1	NERK2_HUMAN
7	530.5	8.5	459	1	NERK2_MOUSE
8	528.5	8.5	431	1	NIMA_EMENT
9	502.5	8.0	1142	1	GIN4_YEAST
10	499.5	8.0	779	1	NIMA_NECR
11	468.5	7.5	966	1	STIO_MOUSE
12	455	7.3	968	1	STIO_HUMAN
13	455	7.2	1518	1	KKK1_YEAST
14	437.5	7.0	915	1	KCC4_YEAST
15	432	6.9	435	1	KIN3_YEAST
16	421.5	6.8	1895	1	KIN3_CAEEL
17	393	6.3	1080	1	NRK1_YEAST
18	388	6.2	1062	1	CCR1_MOUSE
19	383.5	6.1	705	1	CCR1_MOUSE
20	382.5	6.1	740	1	KK63_HUMAN
21	382.5	6.1	740	1	KK63_HUMAN
22	382.5	6.1	740	1	KK63_HUMAN
23	380.5	6.1	682	1	SNK_MOUSE
24	380.5	6.1	682	1	SNK_MOUSE
25	379	6.1	682	1	SNK_MOUSE
26	378	6.1	631	1	SNK_MOUSE
27	378	6.1	631	1	SNK_MOUSE
28	378	6.1	733	1	K6A2_HUMAN
29	378	6.1	733	1	K6A2_HUMAN
30	378	6.1	733	1	K6A2_HUMAN
31	378	6.1	733	1	K6A1_HUMAN
32	377.5	6.0	733	1	K6A1_HUMAN
33	375	6.0	1305	1	GAR_NAT

ALIGNMENTS

RESULT	ID	NEK1_MOUSE	STANDARD	PRT	774 AA.
AC	01-0CT-1996 (Rel. 34, Created)				
DT	01-0CT-1996 (Rel. 34, Last sequence update)				
DT	16-0CT-2001 (Rel. 40, Last annotation update)				
DE	Serine/threonine-protein kinase Nek1 (EC 2.7.1.-) (NIMA-related protein kinase 1).				
GN	NEK1				
OS	NIMA-related (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Blood;				
RA	Levin K., Mizzen L., Motro B., Ben-David Y., Bernstein A., Dawson T.;				
RT	A mammalian dual specificity protein kinase, Nek1, is related to the NIMA cell cycle regulator and highly expressed in meiotic germ cells.;				
EMBO J.	11:3521-3531(1992).				
CC	- FUNCTION: PHOSPHORYLATES SERINES AND THREONINES, BUT ALSO APPEARS TO POSSESS TYROSINE KINASE ACTIVITY. IMPLICATED IN THE CONTROL OF MEIOSIS.				
CC	- SUBCELLULAR LOCATION: Nuclear (Probable).				
CC	- TISSUE SPECIFICITY: PREDOMINANTLY IN TESTES (CPM CELLS AND SPERMATOCYTES), LOWER LEVELS IN OVARY (OVOCYTES AND GRANULOSA CELLS), THYMUS, AND LONG.				
CC	- DEVELOPMENTAL STAGE: IN FEMALE, EXPRESSED AS FOLLICLES ENTER THE SECONDARY STAGE UNTIL OVULATION OCCURS. IN THE MALE REPRODUCTIVE SYSTEM, THE EXPRESSION IS LIMITED TO SPERMATOCYTES AND SPERMATIDS.				
CC	- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	- NIMA SUBFAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	EMBL: S45628; AAA33529.1;				
CC	HSSP: P24841; 1str.				
DR	MGD: M61:97103; Nek1.				
DR	InterPro: IPR000719; Ser_Thr_Kinase.				
DR	InterPro: IPR002390; Ser_Thr_Kinase.				
DR	Pfam: PF00069; PKinase; 1.				
DR	SMART: SMO0220; S_TKc; 1.				
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.				
DR	PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.				
DR	transferase: Serine/threonine-protein kinase; ATP-binding; Mitosis;				
KW	P57874; ratus norv				

34	374.5	6.0	982	1	SOLD_CAEEL	P46549 caenorhabd
35	374	6.0	350	1	KAPQ_HUMAN	P22612 homo sapien
36	374	6.0	615	1	CKR_BAT	O26011 ratus norv
37	374	6.0	745	1	K6A6_HUMAN	O9UK32 homo sapien
38	373.5	6.0	490	1	SPS1_YEAST	P08458 saccharomyc
39	372	6.0	646	1	CKR_HUMAN	O9H4B4 homo sapien
40	371.5	6.0	485	1	K6B2_MOUSE	O921M4 mus musculu
41	371	5.9	371	1	KAP4_BOVIN	P00217 bos taurus
42	371	5.9	350	1	KAP4_HUMAN	O15812 homo sapien
43	371	5.9	444	1	KAPC_DICED	O15812 dictyostell
44	371	5.9	444	1	KAPC_DICED	O15812 dictyostell
45	369.5	5.9	397	1	KAP4_YEAST	P06244 saccharomyc

KM Nucleic protein: Phosphorylation: Cell cycle: Cell division:
 KM Tyrosine protein kinase.
 FT DOMAIN 4 258 PROTEIN KINASE.
 NP_BIND 10 18 ATP (BY SIMILARITY).
 BINDING 33 33 ATP (BY SIMILARITY).
 FT ACT_SITE 128 128 BY SIMILARITY.
 SEQUENCE 774 AA; 88427 MW; 7E5E881ACD06FA CRC64;

Query Match 54.2%; Score 3385; DB 1; Length 774;
 Best Local Similarity 85.5%; Pred. No. 1,2e-118;
 Matches 665; Conservative 45; Mismatches 64; Indels 4; Gaps 3;

QY 1 MEKYLRLKIGSGSPFKALVSTEDGROYIYKEINISMSKERESEEREAVLANMKH 60
 DB 1 MEKYLRLKIGSGSPFKALVSTEDGROYIYKEINISMSKERESEEREAVLANMKH 60
 QY 61 PNIYVRESFEENGSLIYMDYCEGGDLFRINAGVLFQEDQILDFQICLAKH 120
 DB 61 PNIYVRESFEENGSLIYMDYCEGGDLFRINAGVLFQEDQILDFQICLAKH 120
 QY 61 PNIYVRESFEENGSLIYMDYCEGGDLFRINAGVLFQEDQILDFQICLAKH 120
 DB 61 PNIYVRESFEENGSLIYMDYCEGGDLFRINAGVLFQEDQILDFQICLAKH 120
 QY 121 DRKILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 180
 DB 121 DRKILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 180
 QY 121 DRKILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 180
 DB 121 DRKILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 180
 QY 181 NNSGDIWALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 240
 DB 181 NNSGDIWALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 240
 QY 181 NNSGDIWALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 240
 DB 181 NNSGDIWALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 240
 QY 241 RNPDRPSVNSIIEKGFINKRIEFLSPQIAEFELCTKPSKSGSPYAPKRPASGNSI 300
 DB 241 RNPDRPSVNSIIEKGFINKRIEFLSPQIAEFELCTKPSKSGSPYAPKRPASGNSI 300
 QY 241 RNPDRPSVNSIIEKGFINKRIEFLSPQIAEFELCTKPSKSGSPYAPKRPASGNSI 300
 DB 241 RNPDRPSVNSIIEKGFINKRIEFLSPQIAEFELCTKPSKSGSPYAPKRPASGNSI 300
 QY 301 SYMPAKRTKPAKNGCIPLAYKRGDKRLHKKPLQKHKQAOHPTKRNNGEERKRISE 360
 DB 301 SYMPAKRTKPAKNGCIPLAYKRGDKRLHKKPLQKHKQAOHPTKRNNGEERKRISE 360
 QY 301 SYMPAKRTKPAKNGCIPLAYKRGDKRLHKKPLQKHKQAOHPTKRNNGEERKRISE 360
 DB 301 SYMPAKRTKPAKNGCIPLAYKRGDKRLHKKPLQKHKQAOHPTKRNNGEERKRISE 360
 QY 361 EAKARRRLEFEERKKOKQOITSLKKAQMKRKEKLEIRINAROGANVLSAGSGE 420
 DB 361 EAKARRRLEFEERKKOKQOITSLKKAQMKRKEKLEIRINAROGANVLSAGSGE 420
 QY 361 EAKARRRLEFEERKKOKQOITSLKKAQMKRKEKLEIRINAROGANVLSAGSGE 420
 DB 361 EAKARRRLEFEERKKOKQOITSLKKAQMKRKEKLEIRINAROGANVLSAGSGE 420
 QY 421 VAPPLSGGCTIAPSSFSRGQYEHYHIFPMOQOAAEDENKMYREIYGGCLPEKRG 480
 DB 421 VAPPLSGGCTIAPSSFSRGQYEHYHIFPMOQOAAEDENKMYREIYGGCLPEKRG 480
 QY 421 VAPPLSGGCTIAPSSFSRGQYEHYHIFPMOQOAAEDENKMYREIYGGCLPEKRG 480
 DB 421 VAPPLSGGCTIAPSSFSRGQYEHYHIFPMOQOAAEDENKMYREIYGGCLPEKRG 480
 QY 420 VASFFGIGCAVSPSPSGQYEHYHIFPMOQOAAEDENKMYREIYGGCLPEKRG 479
 DB 420 VASFFGIGCAVSPSPSGQYEHYHIFPMOQOAAEDENKMYREIYGGCLPEKRG 479
 QY 481 QLAVERAKOVEEFLQRRKREAMONKARAGHVVYLAIRLOIRLQNFEROQIATKRGSK 540
 DB 481 QLAVERAKOVEEFLQRRKREAMONKARAGHVVYLAIRLOIRLQNFEROQIATKRGSK 540
 QY 481 QLAVERAKOVEEFLQRRKREAMONKARAGHVVYLAIRLOIRLQNFEROQIATKRGSK 540
 DB 481 QLAVERAKOVEEFLQRRKREAMONKARAGHVVYLAIRLOIRLQNFEROQIATKRGSK 540
 QY 541 EAHNSEGQEGSEADMRKRIESTLKAHANAAVLAQLERKREKAYEREKKVMEHIVA 600
 DB 541 EAHNSEGQEGSEADMRKRIESTLKAHANAAVLAQLERKREKAYEREKKVMEHIVA 600
 QY 541 EAHNSEGQEGSEADMRKRIESTLKAHANAAVLAQLERKREKAYEREKKVMEHIVA 600
 DB 541 EAHNSEGQEGSEADMRKRIESTLKAHANAAVLAQLERKREKAYEREKKVMEHIVA 600
 QY 540 EADGTGQGEATEETDMRLKMESTLKAOTNAAVLAQLERKREKAYEREKKVMEHIVA 599
 DB 540 EADGTGQGEATEETDMRLKMESTLKAOTNAAVLAQLERKREKAYEREKKVMEHIVA 599
 QY 601 KGVKSSDVSPPLGQHEGSGSPKQOMRSYISVTSALKVEVDLSLDTRETSEEMOKTN 660
 DB 601 KGVKSSDVSPPLGQHEGSGSPKQOMRSYISVTSALKVEVDLSLDTRETSEEMOKTN 660
 QY 601 KGVKSSDVSPPLGQHEGSGSPKQOMRSYISVTSALKVEVDLSLDTRETSEEMOKTN 660
 DB 601 KGVKSSDVSPPLGQHEGSGSPKQOMRSYISVTSALKVEVDLSLDTRETSEEMOKTN 660
 QY 600 R-VKSSDVPLLELLEGGSPKQOMRSYISVTSALKVEVDLSLDTRETSEEMOKTN 656
 DB 600 R-VKSSDVPLLELLEGGSPKQOMRSYISVTSALKVEVDLSLDTRETSEEMOKTN 656
 QY 661 AISSKREILRLNENLKAODEKQONLSDFEINVEDAKKEHEKKSVSQDRKMEAGC 720
 DB 661 AISSKREILRLNENLKAODEKQONLSDFEINVEDAKKEHEKKSVSQDRKMEAGC 720
 QY 661 AISSKREILRLNENLKAODEKQONLSDFEINVEDAKKEHEKKSVSQDRKMEAGC 720
 DB 661 AISSKREILRLNENLKAODEKQONLSDFEINVEDAKKEHEKKSVSQDRKMEAGC 720
 QY 657 AISSKREILRLNENLKAODEKQONLSDFEINVEDAKKEHEKKSVSQDRKMEAGC 716
 DB 657 AISSKREILRLNENLKAODEKQONLSDFEINVEDAKKEHEKKSVSQDRKMEAGC 716
 QY 721 QLVIPDLDELDTSTFTTERHTVGEVYIKLPGSPRRAMKSPDSEVLAILEAEQL 778
 DB 721 QLVIPDLDELDTSTFTTERHTVGEVYIKLPGSPRRAMKSPDSEVLAILEAEQL 778
 QY 717 QLVIPDLDELDTSTFTTERHTVGEVYIKLPGSPRRAMKSPDSEVLAILEAEQL 774
 DB 717 QLVIPDLDELDTSTFTTERHTVGEVYIKLPGSPRRAMKSPDSEVLAILEAEQL 774

RESULT

STR2_HUMAN STANDARD; PRT: 841 AA.

AC P51957;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Serine/threonine protein kinase 2 (EC 2.7.1.37) (Serine/threonine-
 protein kinase NRK2).
 GN STR2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BREAST;
 RX MEDLINE=34268338; PubMed=8208544;
 RA Levedakou E.N., He M., Baptist E.W., Craven R.J., Cance W.G.,
 Welch P.L., Simons A., Naylor S.L., Leach R.J., Lewis T.B.,
 Bowcock A., Liu E.T.;
 RA "Two novel human serine/threonine kinases with homologies to the cell
 cycle regulating Xenopus M015, and NIMA kinases: cloning and
 characterization of their expression pattern.";
 RT Oncogene 9:1977-1988(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADULT HEART, FOLLOWED BY
 PANCREAS, SKELETAL MUSCLE, BRAIN, LIVER, KIDNEY, LUNG AND
 PLACENTA. PRESENT IN MOST PRIMARY CARCINOMAS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC NIMA SUBFAMILY.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb.ch/announce/>
 or send an email to license@isb.sib.ch).
 CC EMBL: L20321; AAA3658.1;
 CC HSP: P11362; IFGK.
 DR MIM: 601959;
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR SMART: SM00220; S_TKC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM.1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding; Mitosis;
 KM Nucleic protein: Phosphorylation.
 FT DOMAIN 261
 NP_BIND 12 20 ATP (BY SIMILARITY).
 BINDING 35 35 ATP (BY SIMILARITY).
 FT ACT_SITE 131 131 BY SIMILARITY.
 MOD_RES 165 165 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 841 AA; 94571 MW; 0DD31920DDE7EA58 CRC64;

Query Match 13.6%; Score 847.5; DB 1; Length 841;
 Best Local Similarity 28.1%; Pred. No. 5.9e-25;
 Matches 263; Conservative 160; Mismatches 316; Indels 197; Gaps 34;

QY 4 YVRLKIGSGSPFKALVSTEDGROYIYKEINISMSKERESEEREAVLANMKH 63
 DB 4 YVRLKIGSGSPFKALVSTEDGROYIYKEINISMSKERESEEREAVLANMKH 63
 QY 6 YCYLRVKGSGYGVTLVYKRRKQYIYKRLNRSNERRAAEOEOLLSOLKHPNI 65
 DB 6 YCYLRVKGSGYGVTLVYKRRKQYIYKRLNRSNERRAAEOEOLLSOLKHPNI 65
 QY 64 VQYRSEFE-ENGSLIYMDYCEGGDLFRINAGVLFQEDQILDFQICLAKH 122
 DB 64 VQYRSEFE-ENGSLIYMDYCEGGDLFRINAGVLFQEDQILDFQICLAKH 122
 QY 66 VYKESGEGDGLIYMGCEGGDLFRINAGVLFQEDQILDFQICLAKH 125
 DB 66 VYKESGEGDGLIYMGCEGGDLFRINAGVLFQEDQILDFQICLAKH 125
 QY 123 KILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 182
 DB 123 KILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 182
 QY 126 KILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 185
 DB 126 KILHDKSONIFLTQKGTQVLDGFIARVNSTVELARTICIGTPYLSPEICENKPY 185
 QY 183 KSDINALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 242
 DB 183 KSDINALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 242
 QY 186 KSDINALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 245
 DB 186 KSDINALGCVLELCTLKHAFENGSMKLVYKTIISGSPPYSLHYSDRLSYQLFK 245